Zhang et al. Supplementary Figures and Legends

Figure S1. Clusters and patterns of gene expression in uninduced and DOX-induced EBs. A 15K developmental cDNA microarray was screened using RNAs isolated from uninduced versus DOX-induced *i-Mixl1* EBs. The heat map shows expression of genes during differentiation under Dox(+) and Dox(-) conditions. Averaged expression for each time point for each cluster is shown on the right. Gene Ontology (GO) enrichment analysis revealed mesoderm formation genes (*Dkk1, Nckap1, Eomes, Hmga2*) in cluster #8 (see **Table S3**). Exploration of 458 genes for distribution of GO terms containing the words "hematopoiesis" and "blood" also suggested selective enrichment of genes associated with these terms in cluster #8 (*Cdh2, Amot, Gata2, Gas6*).

Figure S2. Expression of Flk1 and Podxl on cells from differentiating EBs. E14 ES cells were induced to differentiate as EBs and harvested at the days indicated. Cells were stained with anti-Flk1 and anti-Podxl1 antibodies and then subjected to flow cytometric analysis.

Figure S3. Expression of *Flk1* and *Podxl* mRNA in differentiating EBs. E14 ES cells were induced to differentiate as EBs and harvested at the days indicated. Total RNA was isolated and analyzed using QRT-PCR. The expression of *Flk1* and *Podxl* was normalized to that of *Gapdh*.

Figure S4. Flow cytometric analysis confirms purity of sorted populations. (A) Flow cytometric analysis showing subdivision of Flk1+ differentiating ES cells based on expression of Podxl in day 4.75 EBs. Boxes represent the gating schematic used to FACS sort each population.

(B) Flow cytometric analysis of each population following sorting. Immediately after sorting, each population was analyzed by flow cytometry to measure sorting efficiency.

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Figure S1

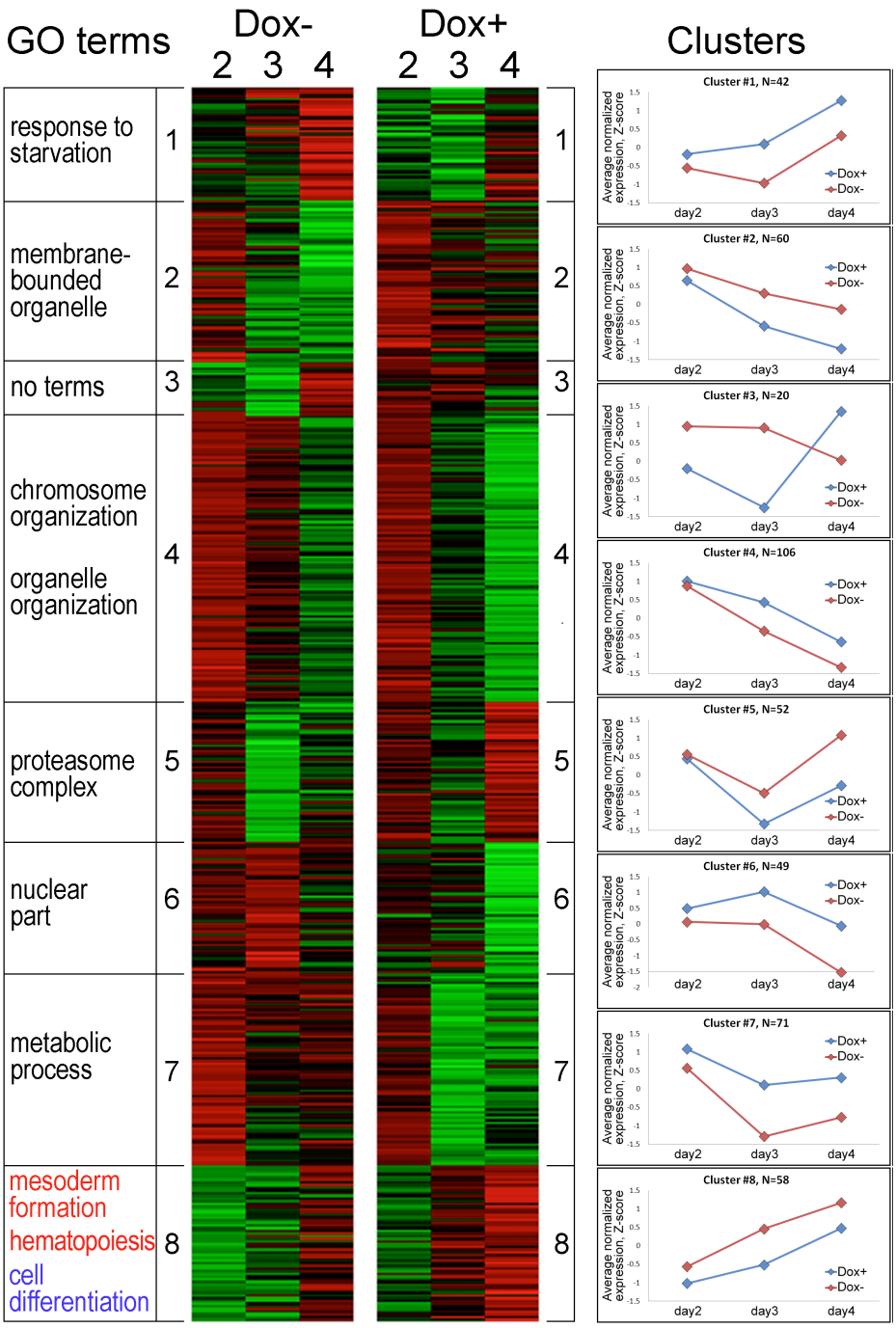

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Figure S2

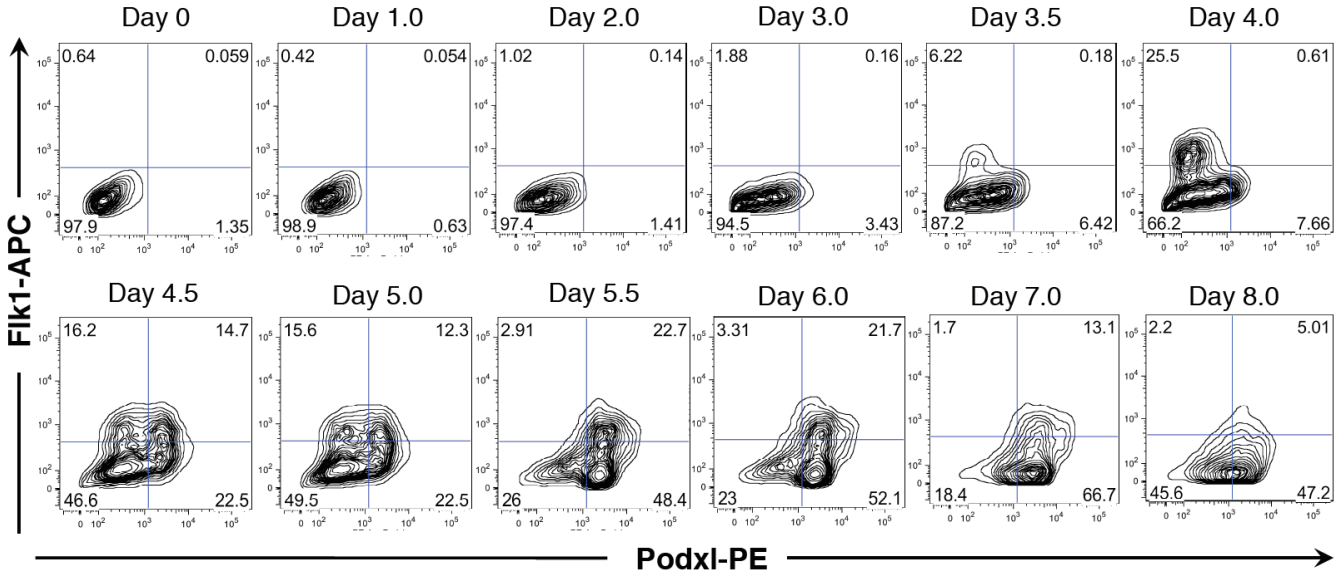

Figure S3

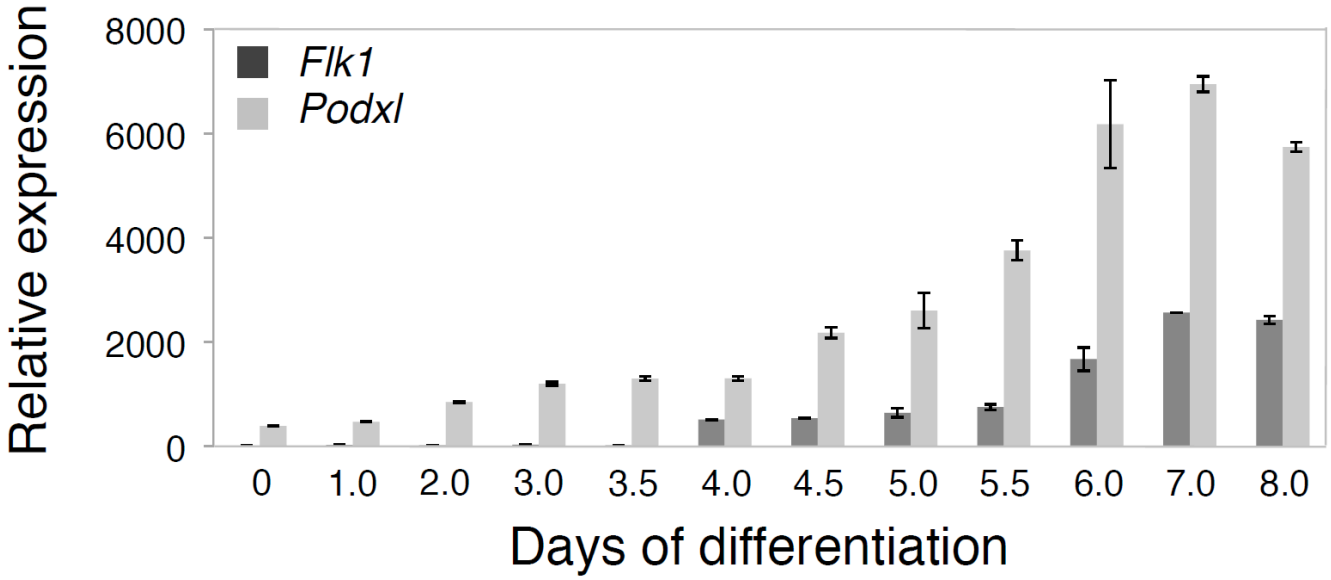

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Figure S4